

Amendments to the Claims

1-13. (Canceled)

14. (Previously Presented) The method of claim 62 wherein the mismatch repair gene is human *PMS2*.

15-18. (Canceled)

19. (Previously Presented) The method of claim 14 wherein said mismatch repair gene comprises a truncation mutation at codon 134 as shown in SEQ ID NO:1.

20. (Original) The method of claim 19 wherein the truncation mutation is a thymidine at nucleotide 424 of wild-type *PMS2* as shown in SEQ ID NO:1.

21-28. (Canceled)

29. (Currently Amended) The hypermutable, ~~nonhuman~~, transgenic ~~mammal mouse~~ of claim 60 comprising a protein which consists of the first 133 amino acids of human *PMS2*.

30-52. (Canceled)

53. (Currently Amended) The hypermutable, ~~nonhuman~~, transgenic ~~mammal~~ mouse of claim 61 wherein the mismatch repair gene is human *PMS2*.

54-57. (Canceled)

58. (Currently Amended) The hypermutable, ~~nonhuman~~, transgenic ~~mammal~~ mouse of claim 61 wherein the dominant negative allele comprises a truncation mutation at codon 134 as shown in SEQ ID NO:1.

59. (Currently Amended) The hypermutable, ~~nonhuman~~, transgenic ~~mammal~~ mouse of claim 58 wherein the truncation mutation is a thymidine at nucleotide 424 of wild-type *PMS2* as shown in SEQ ID NO:1.

60. (Currently Amended) A hypermutable, ~~nonhuman~~, transgenic ~~mammal~~ mouse wherein at least 50% of the cells of said ~~mammal~~ mouse comprise a dominant negative allele of a *PMS2* mismatch repair gene, wherein said dominant negative allele comprises a truncation mutation.

61. (Currently Amended) A hypermutable, ~~nonhuman~~, transgenic ~~mammal~~ mouse produced by a process comprising introducing a polynucleotide comprising a sequence encoding a dominant negative allele of a *PMS2* mismatch repair gene into said ~~mammal~~ mouse, wherein the dominant negative allele comprises a truncation mutation, whereby said ~~mammal~~ mouse becomes hypermutable.

62. (Currently Amended) A method of making a hypermutable, ~~nonhuman, mammalian, murine~~ fertilized egg comprising introducing into said ~~mammalian, murine~~ fertilized egg a polynucleotide comprising a sequence encoding a dominant negative allele of a *PMS2* mismatch repair gene, wherein the dominant negative allele comprises a truncation mutation, whereby said ~~mammalian, murine~~ fertilized egg becomes hypermutable.

63-68. (Canceled)

69. (New) The method of claim 61 wherein the polynucleotide is introduced into a fertilized egg of said mouse.

70. (New) The method of claim 69 wherein the fertilized egg is subsequently implanted into a pseudopregnant female mouse whereby the fertilized egg develops into a mature transgenic mouse.

71. (New) A method for generating a mutation in a gene of interest comprising the steps of:

growing a mouse comprising the gene of interest and a polynucleotide encoding a dominant negative allele of a *PMS2* mismatch repair gene, wherein the dominant negative allele comprises a truncation mutation; and

testing the mouse to determine whether the gene of interest harbors a mutation.

72. (New) The method of claim 71 wherein the step of testing comprises analyzing a nucleotide sequence of the gene of interest.

73. (New) The method of claim 71 wherein the step of testing comprises analyzing mRNA transcribed from the gene of interest.

74. (New) The method of claim 71 wherein the step of testing comprises analyzing a protein encoded by the gene of interest.

75. (New) The method of claim 71 wherein the step of testing comprises analyzing the phenotype of the gene of interest.

76. (New) The method of claim 71 wherein the mouse is made by the process of introducing a polynucleotide comprising a dominant negative allele of a *PMS2* mismatch repair gene into a mouse, whereby the mouse becomes hypermutable.

77. (New) The method of claim 76 wherein the step of testing comprises analyzing a nucleotide sequence of the gene of interest.

78. (New) The method of claim 76 wherein the step of testing comprises analyzing mRNA transcribed from the gene of interest.

79. (New) The method of claim 76 wherein the step of testing comprises analyzing a protein encoded by the gene of interest.

80. (New) The method of claim 76 wherein the step of testing comprises analyzing the phenotype of the gene of interest.